

Figure 2

M A V L G L L F C L V T F P S C
ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA TTC CCA AGC TGT
V L S
GTC CTG TCC (-1 to -19, Leader)

Q V Q V K E S G P F L V P P S Q
CAG GTG CAG GTG AAG GAG TCA GGA CCT TTC CTG GTG CCC CCC TCA CAG
S L S I T C T V S G F S L T
AGC CTG TCC ATC ACA TGC ACT GTC TCA GGG TTC TCA TTA ACC
(1-30, Frame work 1)

T Y G V S
ACC TAT GGT GTA AGC (31-35, CDR 1)

W I R Q P P G K G L E W L G
TGG ATT CGC CAG CCT CCA GGA AAG GGT CTG GAG TGG CTG GGA
(36-49, Frame work 2)

A I W G D G T T N Y H S A L I S
GCA ATT TGG GGT GAC GGG ACC ACA AAT TAT CAT TCA GCT CTC ATA TCC
(50-65, CDR 2)

R L S I S K D N S K S Q V F L K
AGA CTG AGC ATC AGC AAG GAT AAC TCC AAG AGC CAA GTT TTC TTA AAA
L N S L Q T D D T A T Y Y C A K
CTG AAC AGT CTG CAA ACT GAT GAC ACG GCC ACG TAC TAC TGT GCC AAA
(66-97, Frame work 3)

L G N Y D A L D W Y
CTG GGT AAC TAC GAT GCT CTG GAC TAC
(98-106, CDR 3)

W G Q G T S V T V S S
TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
(107-117, Frame work 4)

A K T T P P V Y P L V P G S L
GCC AAA ACG ACA CCC CCA CCC GTC TAT CCA TTG GTC CCT GGA AGC TTG GG
(Constant region)

Figure 3(B)

1A7:	1	QVQVKESGPFLVPPSQSLITCTVSGFSLTGYGVSWIRQPPGKGLEWLGAIWGDGTTNYH	60
1	1	.G..A.....S.....V.....S....	52
2	1	..LQ...G..A.....S..IT.V.....V.....N....	60
3	20	..L...G..A.....G..N.V.....T..N.S.D.N	79
4	1	..L..T..G..A.....S..H.V.....VV..S..S..N	60
5	1	..L...G..A.....S..H.V.....V..AG.S..N	60
6	1	..L...G..A.....S..H.V.....V..AG.S..N	60
7	1	..L...G..A.....P..S..D.V.....V..G.S..N	60
8	23	..LQ...G..A.....G..N.V.....M.....N.D.N	82
9	1	..L...G..A.....G..N.V.....M.....N.D.N	60
10	133	..LQ...G..A.....G..N.V.....M.....N.D.N	192
11	20	..L...G..A.....G..N.V.....M.....N.D.N	79
12	1	..L...G..A.....SR.S.H.V.....M...G.N.D.N	60
13	21	.HL....V..A.....N..H.V.....V..AG.N..N	80
14	23	..LQ...G..A.....G..N.V.....M.....N.D.N	82
15	1	..LQ...G..A.....G..N.V.....M.....N.D.N	60

DYWG

1A7:	61	SALISRLSISKDNSKSQVFLKLNSLQTDATYYCAKL-----GNYDALB BL EQGTSVTVSS	117
1	53P.....YDYExxxxx YTL..	109
2	61x-----xxxxxx.K Y	120
3	80	.T.K..T.T.....M.....R...SVSIYYYGRSDK.FT. Y	144
4	61	..K.....M.....M...Rx-----xx.D.Y.M Y	119
5	61	..M.....M.....M...Rx-----xxxxxx.Y.M Y	120
6	61	..M.....M.....M...Rx-----xxxx.Y.M Y	118
7	61	..M.....M..X..M...xx-----xxx.X.Y.M Y	119
8	83	..K.....M..H..R...RE-----RDYR. Y ...T....	138
9	61	..K.....M..H..R...RE-----RDYR. Y ...TL....	116
10	193	..K.....M..H..R...RE-----RDYR. Y ...T....	248
11	80	..K.....M..H..R...RE-----RDYR. Y ...TL....	135
12	61	..K.....M.....M...RD-----GYYDx.M Y	117
13	81	..M.....M..I..I...x-----xxxxx.Y.M Y	139
14	83	..K.....M..H..R...RE-----RDYR. Y ...T....	138
15	61	..K.....M..H..R...RE-----RDYR. Y ...T....	116

Figure 3(C)

VL consensus:	1	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKQSPKLLIYFVSNRF	60
1A7:	1P....N.....	60

VL consensus:	61	SGVPDRFSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPWTFGGGTKLEIK	112
1A7:	61	112

VH consensus:	1	QVQLKESGPLVAPSQSLSICTVSGFSLTSYGVHWRQPPGKGLEWLGVIWGDGSTYN	60
1A7:	1	...V.....F..P.....T...S.I.....A.....T...H	60

VH consensus:	61	SALKSRLSISKDNKSQVFLKMNSLQTDDTARYYCARExxxxYYAMDYWGQGTSVTVSS	119
1A7:	61	...I.....L.....T....KL--GN.D	117